#gene1	gene2	strand1	strand2	breakpoint1	breakpoint2	site1	site2	type	split_reads1	split_reads2	discordant_mates	coverage1	coverage2	confidence	reading_frame	tags	retained_protein_domains	closest_genomic_breakpoint1	closest_genomic_breakpoint2	gene_id1	gene_id2	transcript_id1	transcript_id2	direction1	direction2	filters	fusion_transcript	peptide_seq	read_identifiers
RPS6KB1	VMP1	+/+	+/+	chr17:59914703	chr17:59839768	CDS/splice-site	CDS/splice-site	duplication	10	11	0	371	569	high	in-frame		Protein_kinase_domain(14%)|	.	.	ENSG00000108443.14	ENSG00000062716.13	ENST00000225577.9	ENST00000262291.9	downstream	upstream	duplicates(39),mismatches(2)	AAAGTAACAGGAGCAAATACTGGGAAAATATTTGCCATGAAGGTGCTTAAAAAG|GGAGAAAACTGGTTGTCCTGGATGTTTGAAAAGTTGGTCGTTGT	KVTGANTGKIFAMKVLKK|GENWLSWMFEKLVVVMV	SRR12576402.10183219,SRR12576402.10382239,SRR12576402.10479224,SRR12576402.10504130,SRR12576402.11761237,SRR12576402.11898525,SRR12576402.120604,SRR12576402.1342170,SRR12576402.14615630,SRR12576
RPS6KB1	VMP1	+/+	+/+	chr17:59912804	chr17:59839768	CDS/splice-site	CDS/splice-site	duplication	1	1	0	466	569	medium	in-frame		Protein_kinase_domain(5%)|	.	.	ENSG00000108443.14	ENSG00000062716.13	ENST00000225577.9	ENST00000262291.9	downstream	upstream	duplicates(1)	GAGCTACTTCGGGTACTTGGTAAAGGGGGCTATGGAAAG|GGAGAAAACTGGTTGTCCTGGATGTTTGAAAAGTTGGTCGTTGT	ELLRVLGKGGYGK|GENWLSWMFEKLVV	SRR12576402.17187310,SRR12576402.13181866,SRR12576402.23021255
ARFGEF2	SULF2	+/+	-/-	chr20:48922010	chr20:47736942	CDS/splice-site	CDS/splice-site	inversion	9	9	0	124	197	high	in-frame	Mitelman	Dimerisation_and_cyclophilin-binding_domain_of_Mon2(10%)|Sulfatase(95%),Sulfatase_protein(100%)	.	.	ENSG00000124198.10	ENSG00000196562.16	ENST00000371917.5	ENST00000698128.1	downstream	downstream	duplicates(47),mismatches(2)	GAGGTGAAGCGGCCCCAGCACTCCCAGCTGCGCAGGGCCTGCCAGGTGGCCGCTCG|GTTCCATGCAGGTGATGAACAAGACCCGGCG	EVKRPQHSQLRRACQVAL|gSMQVMNKTRRIMEQGG	SRR12576402.10091218,SRR12576402.11096894,SRR12576402.1158056,SRR12576402.12421999,SRR12576402.13360089,SRR12576402.15449016,SRR12576402.16110343,SRR12576402.16619679,SRR12576402.16902566,SRR125
NCOA3	ENSG00000270342(36653),ENSG00000270976(198826)	+/+	./+	chr20:47502019	chr1:106581397	5'UTR/splice-site	intergenic	translocation	8	4	0	173	38	high	.	.	.	.	.	ENSG00000124151.19	.	ENST00000371998.8	.	downstream	upstream	duplicates(14)	AGCGGCGAGTTTCCGATTTAAAGCTGAGCTGCGAGGAAAATGGCGGCGGGAG|GTTAGCCACCCAGTAGAGCTACTGAGTTCCATCCTGGTACT	.	SRR12576402.11564024,SRR12576402.15093168,SRR12576402.24404991,SRR12576402.5790677,SRR12576402.8908811,SRR12576402.9744203,SRR12576402.10088204,SRR12576402.10648141,SRR12576402.12368652,SRR12576
USP32	PPM1D	-/-	+/-	chr17:60265412	chr17:60602618	CDS/splice-site	intron	duplication/5'-5'	6	5	0	314	56	high	out-of-frame	.	EF_hand(100%)|	.	.	ENSG00000170832.13	ENSG00000170836.13	ENST00000300896.9	.	upstream	downstream	duplicates(4),mismappers(1)	TATGGATCTCTCTGATATTGTAGAAGGCATACTGAATGCACATGACACCACAAG|CATGGCCCCTGCTTTATTAAAAAATGTTCCTGAAGGTCCG	MDLSDIVEGILNAHDTTK|hgpcfikkcs*	SRR12576402.13335522,SRR12576402.13362992,SRR12576402.13728543,SRR12576402.17361179,SRR12576402.1947785,SRR12576402.21714655,SRR12576402.23671122,SRR12576402.4088114,SRR12576402.5691385,SRR12576
GCN1	MSI1	-/-	-/-	chr12:120190298	chr12:120347514	CDS/splice-site	CDS/splice-site	duplication	7	4	0	115	33	high	in-frame	.	.	.	.	ENSG00000089154.11	ENSG00000135097.7	ENST00000300648.7	ENST00000257552.7	upstream	downstream	duplicates(3),mismatches(1)	GAACGGAGAGAAATCCTCAGTGAACTTGGGAAGTGTGTTGCTGGAAAAG|CCATTCCTCTCACTGCCTACGGACCAATGGCGGCGGCAGCG	ERREILSELGKCVAGK|alPLTAYGPMAAAAAA	SRR12576402.12041118,SRR12576402.16153681,SRR12576402.21893061,SRR12576402.21959351,SRR12576402.2262748,SRR12576402.2309246,SRR12576402.4110081,SRR12576402.6424466,SRR12576402.8199419,SRR125764